SEQUENCE LISTING

<110> Conklin, Darrell C.
Blumberg, Hal

<120> A HUMAN 2-19 PROTEIN HOMOLOGUE, Z219A

<130> 97-63C1

<150> US 60/061,712
<151> 1997-10-06

<150> US 09/167,513
<151> 1998-10-06

<160> 28

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 876
<212> DNA
<213> Homo sapiens

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<222> (119)...(823)

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ctggctgcgg tcgcctggga gctgccgcca gggccaggag gggagcggca cctggaag      118
atg cgc cca ttg gct ggt ggc ctg ctc aag gtg gtg ttc gtg gtc ttc      166
Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val Phe
 1               5                  10                  15

gcc tcc ttg tgt gcc tgg tat tcg ggg tac ctg ctc gca gag ctc att      214
Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu Leu Ile
             20                  25                  30
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cca gat gca ccc ctg tcc agt gct gcc tat agc atc cgc agc atc ggg      262
Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg Ser Ile Gly
        35                  40                  45

gag agg cct gtc ctc aaa gct cca gtc ccc aaa agg caa aaa tgt gac      310
Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg Gln Lys Cys Asp
    50                  55                  60

cac tgg act ccc tgc cca tct gac acc tat gcc tac agg tta ctc agc      358
His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala Tyr Arg Leu Leu Ser
65                  70                  75                  80

gga ggt ggc aga agc aag tac gcc aaa atc tgc ttt gag gat aac cta      406
Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys Phe Glu Asp Asn Leu
                85                  90                  95

ctt atg gga gaa cag ctg gga aat gtt gcc aga gga ata aac att gcc      454
Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg Gly Ile Asn Ile Ala
            100                 105                 110

att gtc aac tat gta act ggg aat gtg aca gca aca cga tgt ttt gat      502
Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala Thr Arg Cys Phe Asp
        115                 120                 125

atg tat gaa ggc gat aac tct gga ccg atg aca aag ttt att cag agt      550
Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr Lys Phe Ile Gln Ser
    130                 135                 140

gct gct cca aaa tcc ctg ctc ttc atg gtg acc tat gac gac gga agc      598
Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr Tyr Asp Asp Gly Ser
145                 150                 155                 160

aca aga ctg aat aac gat gcc aag aat gcc ata gaa gca ctt gga agt      646
Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser
                165                 170                 175

aaa gaa atc agg aac atg aaa ttc agg tct agc tgg gta ttt att gca      694
Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala
            180                 185                 190

gca aaa ggc ttg gaa ctc cct tcc gaa att cag aga gaa aag atc aac      742
Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn
        195                 200                 205
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cac tct gat gct aag aac aac aga tat tct ggc tgg cct gca gag atc      790
His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile
    210                 215                 220

cag ata gaa ggc tgc ata ccc aaa gaa cga agc tgacactgca gggtcctgag    843
Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
225                 230                 235

taaatgtgtt ctgtataaac aaatgcagct gga                                 876
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<210> 2
<211> 235
<212> PRT
<213> Homo sapiens

<400> 2

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Met Arg Pro Leu Ala Gly Gly Leu Leu Lys Val Val Phe Val Val Phe
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Ala Ser Leu Cys Ala Trp Tyr Ser Gly Tyr Leu Leu Ala Glu Leu Ile
            20                  25                  30
Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg Ser Ile Gly
        35                  40                  45
Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg Gln Lys Cys Asp
    50                  55                  60
His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala Tyr Arg Leu Leu Ser
65                  70                  75                  80
Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys Phe Glu Asp Asn Leu
                85                  90                  95
Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg Gly Ile Asn Ile Ala
            100                 105                 110
Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala Thr Arg Cys Phe Asp
        115                 120                 125
Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr Lys Phe Ile Gln Ser
    130                 135                 140
Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr Tyr Asp Asp Gly Ser
145                 150                 155                 160
Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser
                165                 170                 175
Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala
            180                 185                 190
Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn
        195                 200                 205
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His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile
210 215 220
Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser
225 230 235

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<223> Motif 1, corresponding to residues 127 to 129 of SEQ ID NO:2

<400> 3
Phe Asp Met
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<210> 4
<211> 3
<212> PRT
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<220>
<223> Motif 2, corresponding to residues 156 to 158 of SEQ ID NO:2

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Tyr Asp Asp
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<210> 5
<211> 3
<212> PRT
<213> Artificial Sequence

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<223> Motif 3, corresponding to residues 174 to 176 of SEQ ID NO:2

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Leu Gly Ser
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<210> 6
<211> 3
<212> PRT
<213> Artificial Sequence

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<223> Motif 4, corresponding to residues 188 to 190 of SEQ ID NO:2

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Trp Val Phe
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<210> 7
<211> 3
<212> PRT
<213> Artificial Sequence

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<223> Motif 5, corresponding to residues 227 to 229 of SEQ ID NO:2

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Glu Gly Cys
1

<210> 8
<211> 705
<212> DNA
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<221> variation
<222> (1)...(705)
<223> N is any nucleotide

<221> misc_feature
<222> (1)...(705)
<223> n = A,T,C or G

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gcntggtayw snggntayyt nytngcngar ytnathccng aygcnccnyt nwsnwsngcn 120
gcntaywsna thmgnwsnat hggngarmgn ccngtnytna argcnccngt nccnaarmgn 180
caraartgyg aycaytggac nccntgyccn wsngayacnt aygcntaymg nytnytnwsn 240
ggnggnggnm gnwsnaarta ygcnaarath tgyttygarg ayaayytnyt natgggngar 300
carytnggna aygtngcnmg nggnathaay athgcnathg tnaaytaygt nacnggnaay 360
gtnacngcna cnmgntgytt ygayatgtay garggngaya aywsnggncc natgacnaar 420
ttyathcarw sngcngcncc naarwsnytn ytnttyatgg tnacntayga ygayggnwsn 480
acnmgnytna ayaaygaygc naaraaygcn athgargcny tnggnwsnaa rgarathmgn 540
aayatgaart tymgnwsnws ntgggtntty athgcngcna arggnytnga rytnccnwsn 600
garathcarm gngaraarat haaycaywsn gaygcnaara ayaaymgnta ywsnggntgg 660
ccngcngara thcarathga rggntgyath ccnaargarm gnwsn 705

<210> 9
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC695

<400> 9
gatttaggtg acactatag 19

<210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC7231

<400> 10
tttttttttt tttttttttt tttttv 26

<210> 11
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC13695

<400> 11
cccttccgaa attcagagag 20

<210> 12
<211> 20
<212> DNA
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<223> Oligonucleotide primer ZC13789

<400> 12
tccctgccca tctgacacct 20

<210> 13
<211> 20
<212> DNA
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<223> Oligonucleotide primer ZC13790

<400> 13
ccagctgttc tcccataagt 20

<210> 14
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<400> 14
cttggcatcg ttattcagtc t 21

<210> 15
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<223> Oligonucleotide primer ZC13072

<400> 15
aggtcctggg caagtgctgc 20

<210> 16
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<223> Oligonucleotide primer ZC13956

<400> 16
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<210> 17
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<223> Oligonucleotide primer ZC13957

<400> 17
cgatgctgcg gatgctat 18

<210> 18
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> z219aCEE polypeptide with C-terminal GluGlu tag

<400> 18
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20 25 30
Pro Asp Ala Pro Leu Ser Ser Ala Ala Tyr Ser Ile Arg Ser Ile Gly
35 40 45

Glu Arg Pro Val Leu Lys Ala Pro Val Pro Lys Arg Gln Lys Cys Asp
50 55 60
His Trp Thr Pro Cys Pro Ser Asp Thr Tyr Ala Tyr Arg Leu Leu Ser
65 70 75 80
Gly Gly Gly Arg Ser Lys Tyr Ala Lys Ile Cys Phe Glu Asp Asn Leu
85 90 95
Leu Met Gly Glu Gln Leu Gly Asn Val Ala Arg Gly Ile Asn Ile Ala
100 105 110
Ile Val Asn Tyr Val Thr Gly Asn Val Thr Ala Thr Arg Cys Phe Asp
115 120 125
Met Tyr Glu Gly Asp Asn Ser Gly Pro Met Thr Lys Phe Ile Gln Ser
130 135 140
Ala Ala Pro Lys Ser Leu Leu Phe Met Val Thr Tyr Asp Asp Gly Ser
145 150 155 160
Thr Arg Leu Asn Asn Asp Ala Lys Asn Ala Ile Glu Ala Leu Gly Ser
165 170 175
Lys Glu Ile Arg Asn Met Lys Phe Arg Ser Ser Trp Val Phe Ile Ala
180 185 190
Ala Lys Gly Leu Glu Leu Pro Ser Glu Ile Gln Arg Glu Lys Ile Asn
195 200 205
His Ser Asp Ala Lys Asn Asn Arg Tyr Ser Gly Trp Pro Ala Glu Ile
210 215 220
Gln Ile Glu Gly Cys Ile Pro Lys Glu Arg Ser Gly Ser Glu Tyr Met
225 230 235 240
Pro Met Glu

<210> 19
<211> 25
<212> DNA
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<220>
<223> Oligonucleotide primer ZC14870

<400> 19
atcgtaggaa ttcatgcgcc cattg 25

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC15101

<400> 20
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<210> 21
<211> 8
<212> PRT
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<220>
<223> Glu-Glu tag sequence with linker

<400> 21
Gly Ser Glu Tyr Met Pro Met Glu
1 5

<210> 22
<211> 20
<212> DNA
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<220>
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<400> 22
ggctgtcctc taagcgtcac 20

<210> 23
<211> 19
<212> DNA
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<220>
<223> Oligonucleotide primer ZC13007

<400> 23
aggggtcaca gggatgcca 19

<210> 24
<211> 6
<212> PRT

<213> Artificial Sequence

<220>
<223> EE peptide sequence

<400> 24
Glu Tyr Met Pro Val Asp
1 5

<210> 25
<211> 21
<212> DNA
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<220>
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<210> 26
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<211> 32
<212> DNA
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<220>
<223> Oligonucleotide primer ZC17185

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